

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2005, 18:49:35 ; Search time 2981 Seconds

(without alignments)  
2212.543 Million cell updates/sec

Title: US-10-804-491-25

Sequence: 1 MCKGLAALPHSLERAKKX.....MEXDLPFRVSEFYELIK 181

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame\_p2n.model -DEV=xlp  
-Q=cpn2\_1/USPTO.spool\_p/US10804491/runat\_07012005\_093054\_7744/app\_query.fasta\_1.327  
-DB=EST -QFMT=fastap -SUFFIX=est -MIMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdt -LIST=45  
-DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=psco -NORM=DCT -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10804491\_@CGN\_1\_1\_5180\_@runat\_07012005\_093054\_7744 -NCPU=6 -ICPU=3  
-NO MAP -LANG=QUEURY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAPN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.\*  
1: gb\_esc1.\*  
2: gb\_esc2.\*  
3: gb\_hic.\*  
4: gb\_esc3.\*  
5: gb\_esc4.\*  
6: gb\_esc5.\*  
7: gb\_esc6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	583	6	CA773163 im60e01.y
2	931	100.0	584	7	CK818116 ic13d08.x
3	931	100.0	585	6	CA948732 iq27a04.y
4	931	100.0	614	6	CA951023 ic93h02.y
5	931	100.0	631	4	BMS03802
6	931	100.0	632	5	BQ776798 iq96a05.y
7	931	100.0	633	4	CA841290 ip32c06.y
8	931	100.0	641	4	BT173756 ic03f03.y
9	931	100.0	645	6	CA394466 cs51h05.y

10	931	100.0	645	6	CA397513 cs92a10.y
11	931	100.0	651	6	CB053503 NISC.g114
12	931	100.0	653	5	BU785180 iq42509.y
13	931	100.0	661	2	BE890175
14	931	100.0	695	7	CN268954
15	931	100.0	696	1	AU139601
16	931	100.0	708	6	CA407266 1003415 H
17	931	100.0	708	6	CD242148 AGENCOURT
18	931	100.0	714	6	CB962876
19	931	100.0	718	6	CA391795
20	931	100.0	722	6	CB962581
21	931	100.0	733	5	BU539566
22	931	100.0	734	6	CD299504 AGENCOURT
23	931	100.0	734	6	CD357245
24	931	100.0	737	4	BT770010
25	931	100.0	737	6	CD000470
26	931	100.0	738	6	CD299098
27	931	100.0	740	6	CD110719
28	931	100.0	742	7	CN268951
29	931	100.0	744	6	CD511422
30	931	100.0	746	6	CB963796
31	931	100.0	746	6	CD250671
32	931	100.0	748	4	BG708234
33	931	100.0	748	6	CD299067
34	931	100.0	749	1	AU138261
35	931	100.0	751	6	CB962349
36	931	100.0	752	6	CD511204
37	931	100.0	753	6	CB963300
38	931	100.0	756	6	CB963443
39	931	100.0	757	6	CD241903 AGENCOURT
40	931	100.0	759	6	CD356513
41	931	100.0	759	6	CB962257
42	931	100.0	762	6	CD356626
43	931	100.0	763	6	CB963030
44	931	100.0	765	7	CN268950
45	931	100.0	766	6	CB962986

## ALIGNMENTS

RESULT 1  
CA773163  
DEFINITION  
im60e01.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6039624 5' similar to SW:RG85\_HUMAN O15539 REGULATOR OF G-PROTEIN SIGNALING 5' ; mRNA sequence.

ACCESSION  
CA773163  
VERSION  
CA773163.1 GI:26010458

KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 583)

Lenishka, I., Speares, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Maira, M., Pape, D., Wylie, T., Martin, J., Bliscain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T., Jackson, Y., and Bowers, Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@oeb.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue. DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue

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OM protein - nucleic search, using frame\_plus\_pzn model

Run on: January 12, 2005, 20:02:25 ; Search time 446 Seconds

(without alignments)  
2331.852 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931  
Sequence: 1 MCKGALPHSCLEKAEIK.....MEKSLPRVSEFYOLIK 181

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ pzn model -DEV=xlp  
-O=/cgn2\_1/USPTO\_epool\_p/US10804491/runat 07012005 093056 7844/app query.fasta\_1.327  
-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10804491 @CGN 1 1 723 @runat 07012005 093056 7844  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DISPATCH=100  
-LONGLOP=0 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PTCTUS\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PTCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
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- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	744	9 US-09-206-639-2	Sequence 2, Appl1
2	931	100.0	1691	17 US-10-804-491-24	Sequence 24, Appl1
3	931	100.0	1923	15 US-10-411-224-55	Sequence 55, Appl1
4	931	100.0	1923	16 US-10-047-021-55	Sequence 55, Appl1
5	931	100.0	2076	16 US-10-240-425-345	Sequence 345, Appl1
6	931	100.0	2190	16 US-10-641-643-795	Sequence 795, Appl1
7	918	98.6	5809	15 US-10-133-013-103	Sequence 103, Appl1
8	838	90.0	543	15 US-10-398-953-2	Sequence 2, Appl1
9	838	90.0	817	15 US-10-398-953-6	Sequence 6, Appl1
10	661	71.0	663	16 US-10-357-820-47	Sequence 47, Appl1
11	637	68.4	459	10 US-09-918-995-17122	Sequence 17122, A
12	584	62.7	411	10 US-09-918-995-17122	Sequence 1091, Ap
13	499	53.6	800	16 US-10-305-720-1091	Sequence 9863, Ap
14	499	53.6	1531	14 US-10-198-846-9863	Sequence 144, Ap
15	499	53.6	1869	14 US-10-175-523-144	Sequence 13843, A
16	499	53.6	2752	14 US-10-198-846-13843	Sequence 1, Appl1
17	499	53.6	2934	10 US-09-939-209A-1	Sequence 113, App
18	499	53.6	3165	13 US-10-044-090-113	Sequence 201, App
19	499	53.6	3167	10 US-09-918-624B-6	Sequence 311, App
20	463.5	49.8	2383	14 US-10-171-311-201	Sequence 7, Appl1
21	463.5	49.8	2383	16 US-10-159-563-311	Sequence 112, App
22	462.5	49.7	746	9 US-09-873-438-3	Sequence 606, App
23	462.5	49.7	875	15 US-10-755-889-7	Sequence 353, App
24	462.5	49.7	2434	15 US-10-240-965-112	Sequence 1, Appl1
25	462.5	49.7	2883	18 US-10-723-860-666	Sequence 1721, Ap
26	461	49.5	939	16 US-10-302-172-353	Sequence 1957, A
27	459	49.3	540	15 US-10-875-555-1	Sequence 1955, Ap
28	447	48.0	2272	9 US-09-873-438-1	Sequence 1040, Ap
29	445.5	47.9	1697	15 US-10-094-749-11	Sequence 13, Appl1
30	444.5	47.7	3594	13 US-10-087-192-1727	Sequence 1090, Ap
31	443	47.6	1283	16 US-10-087-192-1727	Sequence 1426, Ap
32	440.5	47.3	2623	16 US-09-814-353-19578	Sequence 5665, Ap
33	440.5	47.3	2638	9 US-09-954-456-1955	Sequence 847, App
34	440.5	47.3	2638	16 US-10-108-260A-1527	Sequence 244, App
35	440.5	47.3	2638	16 US-09-954-456-1955	Sequence 1995, Ap
36	440.5	47.3	2638	16 US-10-428-487-13	Sequence 1527, Ap
37	440.5	47.3	2638	16 US-10-305-720-1090	Sequence 1527, Ap
38	440.5	47.3	2638	16 US-10-240-425-1426	Sequence 1527, Ap
39	427.5	45.9	1164	9 US-10-723-860-666	Sequence 1527, Ap
40	423	45.4	2874	16 US-09-894-749-3	Sequence 1527, Ap
41	421.5	45.3	848	9 US-10-114-270-151	Sequence 1527, Ap
42	421.5	45.3	1629	16 US-09-867-550-847	Sequence 1527, Ap
43	421.5	45.3	1629	16 US-10-191-803-244	Sequence 1527, Ap
44	421.5	45.3	1840	16 US-10-152-312A-1995	Sequence 1527, Ap
45	421.5	45.3	1884	17 US-10-258-371B-18	Sequence 1527, Ap

## ALIGNMENTS

RESULT 1  
US-09-206-639-2  
Sequence 2, Application US/09206639  
Patent No. US20020034777A1

GENERAL INFORMATION:  
APPLICANT: Hiltman, Jennifer L.

TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Potter Drive  
CITY: Palo Alto  
STATE: CA

COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2005, 19:08:15 ; Search time 87 Seconds  
(without alignment)  
1478,768 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931  
Sequence: 1 MCKGLAAPHSCLEPRAXIK.....NEKSLPRFVSEPEYQELIK 181

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO\_spool\_p/US10804491/rnat 07012005 093055 7757/app query.fasta\_1.327  
-DB=Issued Patents NA -QFMT=fastp -SUFFIX=rmi -MINMATCH=0.1 -IOOPT=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10804491@cgn2\_1.1.105@rnat 07012005 093055 7757 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DISPATCH=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/6C.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	744	2	US-08-748-483-2
2	931	100.0	1691	4	US-09-709-103-24
3	931	100.0	1691	4	US-09-439-410A-24
4	931	100.0	1290	4	US-09-023-655-795
5	918	98.6	3208	4	US-09-566-921-111
6	499	53.6	800	4	US-09-016-434-1091
7	463.5	49.8	2383	1	US-08-274-318-1
8	463.5	49.8	2383	2	US-08-754-108-1
9	462.5	49.7	606	2	US-08-463-081B-27
10	462.5	49.7	606	2	US-08-461-379A-27
11	462.5	49.7	606	2	US-08-462-390B-27
12	462.5	49.7	606	3	US-08-463-074B-27

13	462.5	49.7	606	3	US-08-465-585C-27	Sequence 27, Appl
14	462.5	49.7	606	3	US-08-652-446-27	Sequence 27, Appl
15	462.5	49.7	746	3	US-08-870-815-3	Sequence 3, Appl
16	462.5	49.7	746	3	US-08-949-004-3	Sequence 3, Appl
17	462.5	49.7	2406	2	US-08-463-081B-1	Sequence 1, Appl
18	462.5	49.7	2406	2	US-08-461-379A-1	Sequence 1, Appl
19	462.5	49.7	2406	2	US-08-462-390B-1	Sequence 1, Appl
20	462.5	49.7	2406	2	US-08-463-074B-1	Sequence 1, Appl
21	462.5	49.7	2406	3	US-08-465-585C-1	Sequence 1, Appl
22	462.5	49.7	2406	3	US-08-652-446-1	Sequence 1, Appl
23	461	49.5	939	4	US-09-799-451-353	Sequence 353, App
24	447	48.0	2272	2	US-08-728-228-1	Sequence 1, Appl
25	447	48.0	2272	3	US-08-870-815-1	Sequence 1, Appl
26	447	48.0	2272	3	US-08-949-004-1	Sequence 1, Appl
27	440.5	47.3	2638	4	US-09-016-434-1090	Sequence 1090, Ap
28	427.5	45.9	1164	4	US-09-244-314-3	Sequence 3, Appl
29	427.5	45.9	1164	4	US-09-498-959-1	Sequence 3, Appl
30	421.5	45.3	2217	3	US-09-244-314-1	Sequence 1, Appl
31	421.5	45.3	2217	4	US-09-498-959-1	Sequence 1, Appl
32	415.5	44.6	1345	4	US-09-016-434-1278	Sequence 1278, Ap
33	415.5	44.6	1345	4	US-09-023-655-1243	Sequence 1243, Ap
34	351.5	37.8	1398	4	US-09-016-434-1290	Sequence 1290, Ap
35	351.5	37.8	1398	4	US-09-702-705-322	Sequence 322, App
36	351.5	37.8	1398	4	US-09-736-457-322	Sequence 322, App
37	351.5	37.8	1398	4	US-09-614-148-322	Sequence 322, App
38	351.5	37.8	1398	4	US-09-671-335-322	Sequence 322, App
39	351.5	37.8	1398	4	US-09-589-184-322	Sequence 322, App
40	351.5	37.8	1398	4	US-09-658-824-322	Sequence 322, App
41	318	34.2	981	2	US-08-829-110-2	Sequence 2, Appl
42	318	34.2	981	4	US-09-016-434-240	Sequence 240, App
43	309	33.2	201	2	US-08-588-258B-20	Sequence 20, Appl
44	309	33.2	201	3	US-08-460-505-20	Sequence 20, Appl
45	309	33.2	201	5	PCT-US96-08295-20	Sequence 20, Appl

#### ALIGNMENTS

RESULT 1  
US-08-748-483-2  
Sequence 2, Application US/08748483  
Patent No. 5955314  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,483  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0157 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2005, 18:40:14 ; Search time 2732 Seconds

(without alignment)  
3133.029 Million cell updates/sec

Title: US-10-804-491-25

Sequence: 1 MCKGLAALPHSCLERAKK.....MEKSLPRFVSEFQELIK 181

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame\_plus\_p2n.model -DEV=xlp  
-O=/cgn2.1/USPTO\_spool\_p/US10804491/runat\_07012005\_093054\_7731/app\_query.faeta\_1.327  
-DB=genemb1 -OEMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOEXT=0 -LOOEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biocsum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10804491@cgn2.1 1.5600 @runat\_07012005\_093054\_7731 -NCPU=6 -ICPU=3  
-NO MAP -LARGESQUEERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmb1.\*  
1: gb\_da.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_pi.\*  
8: gb\_pi.\*  
9: gb\_pi.\*  
10: gb\_pi.\*  
11: gb\_pi.\*  
12: gb\_pi.\*  
13: gb\_pi.\*  
14: gb\_pi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	931	100.0	546	AF493929 Homo sapi
2	931	100.0	744	AR075100 Sequence
3	931	100.0	744	BD091623 Human reg
4	931	100.0	1285	AF030108 Homo sapi

5	931	100.0	1691	AF159570
6	931	100.0	1710	BC030059
7	931	100.0	1923	BD074349
8	931	100.0	2075	CO714475
9	931	100.0	2076	AB008109
10	931	100.0	2190	AB080250
11	931	100.0	2601	BV180396
12	931	100.0	5683	HSMB05729
13	918	98.6	3208	AR454638
14	915	98.3	955	BD021618
15	915	98.3	955	BD101556
16	855	91.8	2078	SSC549925
17	843	90.5	1812	BC037683
18	838	90.0	543	BD183821
19	838	90.0	546	BD168778
20	838	90.0	546	AF241259
21	838	90.0	817	BD183825
22	838	90.0	817	BD168782
23	833	89.5	2397	MM067188
24	788	84.6	1219	EX931079
25	767	82.4	4487	BC077275
26	680.5	73.1	2765	BC054594
27	510	54.8	2112	BX950639
28	499	53.6	618	AF493928
29	499	53.6	618	BT007025
30	499	53.6	618	BT007756
31	499	53.6	800	AR270528
32	499	53.6	800	HSU27768
33	499	53.6	840	CO714476
34	499	53.6	1238	CO434203
35	499	53.6	1869	BC000737
36	499	53.6	2753	BC051869
37	499	53.6	2934	AX451335
38	497	53.4	1489	RNU27767
39	497	53.4	2919	AF117211
40	496.5	53.3	2214	AY297457
41	494	53.1	2114	BC055293
42	494	53.1	2781	BC003882
43	491	52.7	630	AB004315
44	473.5	50.9	1651	BC064234
45	468.5	50.3	606	MMU70427

## ALIGNMENTS

RESULT 1	AF493929	546 bp	mRNA	linear	PRI 14-APR-2002
LOCUS	AF493929	546 bp	mRNA	linear	PRI 14-APR-2002
DEFINITION	Homo sapiens regulator of G protein signalling 5 (RGSS5) mRNA,				
ACCESSION	AF493929				
VERSION	AF493929.1	GI:20147750			
KEYWORDS	complete cds.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Regulator of G protein signalling 5 (RGSS5), human				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 546)				
AUTHORS	Publ.H.L. Iii, Ikeda,S.R. and Aronstam,R.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAR-2002) CDNA Resource Center, Guthrie Research				
FEATURES	Institute, One Guthrie Square, Sayre, PA 18840, USA				
SOURCE	Location/Qualifiers				
	1..546				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:550112"				
	1..546				

gene

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2005, 18:39:04 ; Search time 421 Seconds  
(without alignments)  
2256.877 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931  
Sequence: 1 MCKGAALPHSLERAEIK.....MCKSLPRFVSEFYOLIK 181

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=fixme+ p2n.model -DEV=xlp  
-Q/cg2.1/USPTO.spool.p/US10804491/runat.07012005.093053.7724/app.query.fasta.1.327  
-DB=N.Geneseq.23Sep04 -QFMT=fstap -SUFFIX=mg -MINMATCH=0 -LOOPT=0  
-LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10804491 @CGN 1.1 708 @runat.07012005.093053.7724 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N.Geneseq.23Sep04:.\*  
1: geneseqn19808:.\*  
2: geneseqn19908:.\*  
3: geneseqn20008:.\*  
4: geneseqn20018:.\*  
5: geneseqn20018:.\*  
6: geneseqn20028:.\*  
7: geneseqn20028:.\*  
8: geneseqn20038:.\*  
9: geneseqn20038:.\*  
10: geneseqn20038:.\*  
11: geneseqn20038:.\*  
12: geneseqn20048:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	745	2	AAV38084 Human reg
2	931	100.0	1691	3	AA236910 CDNA enco
3	931	100.0	1923	3	AA51745 DNA enco
4	931	100.0	1923	6	ABO92597 Human sec
5	931	100.0	2075	10	ABX74396 Human CDN
6	931	100.0	2076	11	ADP65641 Human mRNA

7	931	100.0	2076	11	ADP65077 Human reg
8	931	100.0	2190	11	AD131469 Human CDN
9	918	98.6	3208	12	AD161743 Human CDN
10	918	98.6	5809	10	AD102562 Human CDN
11	915	98.3	955	4	AA197781 Human neu
12	838	90.0	543	6	AB199975 Rat disea
13	838	90.0	917	6	AB199979 Rat disea
14	661	71.0	663	10	ADP44700 Human NOV
15	645	69.3	663	12	AD050885 Human NOV
16	637	68.4	459	9	ACH26489 Human adu
17	584	62.7	411	9	ACH29910 Human tes
18	499	53.6	753	11	ACH95589 Human BEC
19	499	53.6	800	10	ACA56493 Human sig
20	499	53.6	800	12	AD156289 Human pol
21	499	53.6	1238	4	AA126766 Human bre
22	499	53.6	2769	12	ADP21408 Gene RGS4
23	499	53.6	2934	6	ABK47336 CDNA enco
24	499	53.6	3165	8	ABX63113 Human CDN
25	499	53.6	3167	10	ADBD12660 Human CDN
26	496	53.3	558	10	ADB57446 Toxicity
27	463.5	49.8	2383	8	AA114148 p53 reppo
28	463.5	49.8	2383	8	ACP12929 Human cer
29	463.5	49.8	2383	10	ADK61425 Ovarian C
30	463.5	49.8	2383	11	ADN95175 Human BEC
31	463.5	49.8	2383	12	ADOL9709 Human PRO
32	463.5	49.8	2383	12	ADOL9707 Human PRO
33	462.5	49.7	606	3	AAA39678 Cytochrome
34	462.5	49.7	746	2	AAV34780 Human RAT
35	462.5	49.7	2132	12	ADP21402 Gene RGS1
36	462.5	49.7	2406	2	AA143376 Human cyt
37	462.5	49.7	2406	3	AA39660 Human CRI
38	462.5	49.7	2434	6	AA594857 Human DNA
39	462.5	49.7	2883	12	ADQ23786 Human sof
40	461	49.5	939	6	AB11471 Human pol
41	461	49.5	939	12	ADMA4389 Novel hum
42	459	49.0	540	6	ABR92505 Human reg
43	456	48.3	597	5	AA57422 Human RGS
44	455	48.9	2272	2	AAV34779 Mouse RAT
45	445.5	47.9	1697	10	ADA52443 Human cod

## ALIGNMENTS

RESULT 1	AAV38084	standard; CDNA; 745 BP.
ID	AAV38084	
XX	AAV38084	
AC	AAV38084	
XX	AAV38084	
DT	14-SEP-1998	(first entry)
XX	14-SEP-1998	
DE	Human regulator of G-protein signalling encoding CDNA.	
XX	Human, regulator; G-protein signalling; HRGS; cancer; inflammation;	
KW	hypertension; cardiovascular shock; arrhythmias; asthma; ss.	
XX	Human sapiens.	
OS	Human sapiens.	
XX	Human sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	70..615
FT	CDS	/product="regulator of G-protein signalling"
PD	MO9820128-A1.	
XX	14-MAY-1998.	
PF	06-NOV-1997;	97WO-US018476.
XX	08-NOV-1996;	96US-00748483.
PR	(INCY-) INCYTE PHARM INC.	
XX		
XX		

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:32:21 ; Search time 74.0455 Seconds  
(without alignments)  
1406.471 Million cell updates/sec

Title: US-10-804-491-25  
Perfect score: 931  
Sequence: 1 MCKGLALPHSCLEPRAKEIK.....MEKDSLPRVSEFYQELIK 181

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_tramb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	931	100.0	181	1	RGSS_HUMAN
2	931	100.0	181	2	CAD97669
3	855	91.8	181	2	O86422
4	843	90.5	181	1	RGSS_MOUSE
5	843	90.5	181	2	BAC31773
6	843	90.5	181	2	BAC35555
7	838	90.0	181	1	RGSS_RAT
8	767	82.4	181	2	O6DE67
9	680.5	73.1	182	2	O72D3
10	499	53.6	205	1	RGSS_HUMAN
11	499	53.6	205	2	AAP35671
12	497	53.4	205	1	RGSS_RAT
13	496.5	53.3	205	2	O7S2C6
14	494	53.1	205	2	AAP35293
15	494	53.1	205	2	BAC27009
16	494	53.1	205	2	BAC30249
17	491	52.7	205	1	RGSS_MOUSE
18	473.5	50.9	205	2	O6P3T0
19	473.5	50.9	205	2	AAP64234
20	462.5	49.7	202	1	RGSS_HUMAN
21	462.5	49.7	202	1	AAP35284
22	461.5	49.6	202	1	RGSS_HUMAN
23	459	49.3	180	1	RGSS_MOUSE
24	459	49.3	180	2	AAP65677
25	456.5	49.0	204	2	O939D9
26	456	49.0	180	1	RGSS_RAT
27	456	49.0	198	2	AAP69718
28	455	48.9	201	1	RGSS_MOUSE
29	455	48.9	201	2	O7TN09
30	455	48.9	201	2	BAC37678
31	453	48.7	174	2	O6D610

32	452	48.5	180	2	O8BXT1	O8BXT1 mus musculus
33	452	48.5	180	2	AAP65056	AAP65056 mus musculus
34	451	48.4	199	1	RGSS_RAT	P55700 ratu
35	449	48.2	196	2	O95K68	O95K68 macaca fasc
36	445.5	47.9	192	2	O8WV59	O8WV59 homo sapien
37	445.5	47.9	284	2	O6NV55	O6NV55 homo sapien
38	443.5	47.6	174	2	O8WV02	O8WV02 homo sapien
39	443.5	47.6	319	2	O8NPN6	O8NPN6 homo sapien
40	440.5	47.3	519	1	RGSS_HUMAN	P49796 homo sapien
41	440.5	47.3	917	2	O8TU01	O8TU01 homo sapien
42	440.5	47.3	917	2	O8WFA4	O8WFA4 homo sapien
43	440.5	47.3	917	2	O8WXA0	O8WXA0 homo sapien
44	440.5	47.3	1093	2	O8NPN5	O8NPN5 homo sapien
45	440.5	47.3	1198	2	O6ZRM5	O6ZRM5 homo sapien

## ALIGNMENTS

RESULT 1  
RGSS\_HUMAN STANDARD: PRT: 181 AA.  
AC O15539;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Regulator of G-protein signaling 5 (RGSS).  
GN Name=RGSS;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chatterjee T.K., Fisher R.A.,  
RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Neuroblastoma;  
RX MEDLINE=98419174; PubMed=9747037;  
RA Seki N., Sugano S., Suzuki Y.-I., Nakagawara A., Ohira M.,  
RT Muramatsu M.-A., Saito T., Hori T.,  
RL "Isolation, tissue expression, and chromosomal assignment of human  
RGSS, a novel G-protein signaling regulator gene.";  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=99403338; PubMed=10471929;  
RA Cierniewski M.J., Takesono A., Ma C., Lizano J.S., Xie X.,  
RT Fuernkrantz H., Lanier S.M., Duzic E.,  
RL "Genetic screens in yeast to identify mammalian nonreceptor modulators  
of G-protein signaling.";  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Pull R.L., Ili, Ikeda S.R., Aronson R.S.,  
RT "cDNA clones of human proteins involved in signal transduction  
sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RT Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RL Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RL Dictencko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stedelman M., Soares M.B., Bonaldi M.F., Casavant T.L., Schleez T.E.,  
RP Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Roosa S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:38:13 ; Search time 18.0216 Seconds  
(without alignments)  
966.351 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931  
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSFYQELIK 181

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : PIR 79:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	81.4	181	2 JC7228	G-protein signalin
2	499	53.6	205	2 S78221	G-protein signalin
3	440.5	47.3	519	2 S78089	G-protein signalin
4	415.5	44.6	211	2 IS3020	G-0/G-1 switch reg
5	349.5	37.5	156	2 S43436	B cell activation
6	297	31.9	244	2 T13580	hypothetical prote
7	294	31.6	251	2 S43576	COSB5.7 protein (c
8	294	31.6	254	2 G88571	protein COSB5.7 [i
9	287	30.8	181	2 T21035	hypothetical prote
10	282	30.3	533	2 T31002	hypothetical prote
11	281	30.2	159	2 T21034	hypothetical prote
12	255.5	27.4	173	2 S71812	RGS10 protein - hu
13	232.5	25.0	544	2 JC5503	G-protein signalin
14	222	23.8	558	2 T21468	hypothetical prote
15	214	23.0	234	2 T26672	hypothetical prote
16	213	22.9	473	2 T19337	hypothetical prote
17	197.5	21.2	1367	2 JC5502	G-protein signalin
18	196.5	21.1	832	2 T08422	negative regulator
19	165	17.7	270	2 T22213	hypothetical prote
20	162.5	17.5	274	2 T22214	hypothetical prote
21	159	17.1	838	2 T08423	Axin homolog Ax11
22	150	16.1	719	2 S60771	developmental regu
23	149	16.0	303	2 T29513	hypothetical prote
24	141.5	15.2	235	2 F89472	protein ZC53.7 [im
25	134.5	14.4	284	2 T15700	hypothetical prote
26	127.5	13.7	309	2 S61665	probable membrane
27	114	12.2	229	2 A89473	protein F52D2.2 [i
28	105	11.3	1260	2 T20487	hypothetical prote
29	101.5	10.9	657	2 H86344	T2111.1 protein -

30	101	10.8	1620	2 S61535	nucleotide-binding
31	98.5	10.6	492	2 A61382	phosphorylation re
32	98	10.5	913	2 T31497	hypothetical prote
33	96.5	10.4	1085	2 C96797	unknown protein [i
34	96	10.3	688	1 JC1469	beta-adrenergic-re
35	94	10.1	507	2 C82901	conserved hypothet
36	93	10.0	157	2 G64540	hypothetical prote
37	93	10.0	400	2 E70318	hypothetical prote
38	93	10.0	465	2 D81312	hypothetical prote
39	93	10.0	688	1 A39336	beta-adrenergic-re
40	92.5	9.9	367	2 E81060	conserved hypothet
41	92.5	9.9	395	2 E81805	hypothetical prote
42	92.5	9.9	1046	2 A86790	ATP-dependent dADN
43	91.5	9.8	688	1 T73628	beta-adrenergic-re
44	90	9.7	728	2 A81385	probable ATP /GTP
45	89.5	9.6	2774	2 A43359	microtubule-associ

#### ALIGNMENTS

##### RESULT 1

UC7228  
G-protein signaling regulator 5 homolog - clawed frog  
C/Species: Xenopus sp. (Clawed frog)  
C/Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 21-Jul-2000  
C/Accession: JC7228; PC7066  
R.Saitoh, O.; Odagiri, M.; Masuno, I.; Nomoto, S.; Kinoshita, N.  
Biochem. Biophys. Res. Commun. 270, 34-39, 2000  
A/Title: Molecular cloning and characterization of Xenopus RGS5.  
A/Reference number: JC7228  
A/Accession: JC7228  
A/Molecule type: mRNA  
A/Residues: 1-181 <SAI>  
A/Cross-references: DDBJ:AB038436  
A/Accession: PC7066  
A/Molecule type: protein  
A/Residues: 88-168 <SA2>  
A/Experimental source: embryo  
C/Comment: This protein has function as a GTPase-activating protein. It interacts with  
genesis and cell differentiation.  
C/Superfamily: B-cell activation protein BL34  
C/Keywords: differentiation; embryo

Query Match	81.4%; Score 758; DB 2; Length 181;
Best Local Similarity	79.0%; Pred. No. 4.4e-52;
Matches 143; Conservative	20; Mismatches 18; Indels 0; Gaps 0;
QY	1 MCKGLAALPHSCLERAKEIKITGLILQKPDVGLVFPNKEPKPATQTSIDELAQ 60
DB	1 MCKGLAALPHSCLERAKEIKITGLILQKPDVGLVFPNKEPKPATQTSIDELAQ 60
QY	61 WRDSLDKILNNYGLASPKSPFKSEPESENLSEFWIACEDYKKIKSPAKVAEKAKOYIEEF 120
DB	61 WRDSLEKLNSYGLSVFOSFLKSEPESENLSEFWIACEDYKKIKSPAKVAEKAKOYIEEF 120
QY	121 IQTEAPKEVINIHFTKDTIMKNLVSPSSFDMAQKRIHALMEKDSLPRFVRSFYQELI 180
DB	121 IQTEAPKEVINIHFTKDTIMKNLVSPSSFDMAQKRIHALMEKDSLPRFVRSFYQELI 180
QY	181 K 181
DB	181 K 181

##### RESULT 2

S78221  
G-protein signaling regulator RGP4 - human  
N/Alternate names: G-protein signaling regulator RGS4  
C/Species: Homo sapiens (man)  
C/Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C/Accession: S78221; S66509  
R.Druet, K.



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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:34:53 ; Search time 436.829 Seconds  
(without alignments)  
149.700 Million cell updates/sec

Title: US-10-804-491-25

Sequence: 1 MCKGALAPHSCLERAKEIK.....MEXDISPRVSEFYQELIK 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	181	9	US-09-206-639-1
2	931	100.0	181	15	US-10-258-371B-22
3	931	100.0	181	16	US-10-804-491-25
4	931	100.0	190	14	US-10-411-224-197
5	931	100.0	190	15	US-10-047-021-197
6	838	90.0	181	14	US-10-398-953-1
7	661	71.0	135	15	US-10-357-820-48
8	499	53.6	205	9	US-09-206-639-5
9	499	53.6	205	10	US-09-939-209A-2
10	499	53.6	205	15	US-10-258-371B-21
11	463.5	49.7	202	14	US-10-171-311-202
12	462.5	49.7	202	9	US-09-873-438-4
13	462.5	49.7	202	16	US-10-755-889-8

14	462.5	49.7	204	15	US-10-258-371B-23	Sequence 23, Appl
15	459	49.3	180	14	US-10-275-555-2	Sequence 2, Appl
16	456	49.0	180	15	US-10-258-371B-27	Sequence 27, Appl
17	447	48.0	201	9	US-09-873-438-2	Sequence 2, Appl
18	445.5	47.9	284	14	US-10-094-749-1650	Sequence 1650, Ap
19	444.5	47.7	776	13	US-10-087-192-1728	Sequence 1728, Ap
20	440.5	47.3	519	14	US-10-113-794A-2	Sequence 2, Appl
21	440.5	47.3	519	15	US-10-428-487-14	Sequence 14, Appl
22	440.5	47.3	519	15	US-10-258-371B-28	Sequence 28, Appl
23	440.5	47.3	591	15	US-10-108-260A-3970	Sequence 3970, Ap
24	429.5	46.1	930	14	US-10-113-794A-1	Sequence 1, Appl
25	427.5	45.9	235	9	US-09-894-749-4	Sequence 4, Appl
26	423	45.4	923	15	US-10-114-270-152	Sequence 152, App
27	421.5	45.3	227	9	US-09-867-550-848	Sequence 848, App
28	421.5	45.3	235	9	US-09-894-749-2	Sequence 2, Appl
29	421.5	45.3	235	15	US-10-258-371B-20	Sequence 20, Appl
30	415.5	44.6	211	9	US-09-206-639-4	Sequence 4, Appl
31	415.5	44.6	211	15	US-10-258-371B-24	Sequence 24, Appl
32	415.5	44.6	211	16	US-10-408-765A-493	Sequence 493, App
33	415.5	44.6	220	9	US-09-925-300-1507	Sequence 1507, Ap
34	391	42.0	128	15	US-10-352-843-1	Sequence 1, Appl
35	391	42.0	128	15	US-10-352-843-1	Sequence 1, Appl
36	391	42.0	167	10	US-09-942-055A-1	Sequence 1, Appl
37	351.5	37.8	196	9	US-09-206-639-3	Sequence 3, Appl
38	351.5	37.8	196	9	US-09-736-457-339	Sequence 339, App
39	351.5	37.8	196	9	US-09-902-941-339	Sequence 339, App
40	351.5	37.8	196	9	US-09-849-626-339	Sequence 339, App
41	351.5	37.8	196	10	US-09-476-300-339	Sequence 339, App
42	351.5	37.8	196	14	US-10-017-754-339	Sequence 339, App
43	351.5	37.8	196	14	US-10-113-872-339	Sequence 339, App
44	351.5	37.8	196	14	US-10-247-671-176	Sequence 176, App
45	351.5	37.8	196	14	US-10-283-017-339	Sequence 339, App

## ALIGNMENTS

RESULT 1  
US-09-206-639-1  
Sequence 1, Application US/09206639  
Patent No. US20020034777A1  
GENERAL INFORMATION:  
APPLICANT: Hallman, Jennifer L.  
Goli, Surya K.  
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/206,639  
FILING DATE: 07-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/748,483  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0157 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX: <Unknown>



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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:15:29 ; Search time 23.147 Seconds  
(without alignments)  
519.304 Million cell updates/sec

Title: US-10-804-491-25  
Perfect score: 931  
Sequence: 1 MCKGALPHSCLERAKKIK.....MEKSLPRFRSEFYQELIK 181

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	181	2	US-08-748-483-1
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3	931	100.0	181	4	US-09-439-410A-25
4	607	65.2	120	3	US-08-890-865A-12
5	499	53.6	205	2	US-08-829-110-6
6	499	53.6	205	2	US-08-748-483-5
7	463.5	49.8	202	1	US-08-274-318-2
8	463.5	49.8	202	2	US-08-754-108-2
9	462.5	49.7	202	2	US-08-463-081B-2
10	462.5	49.7	202	2	US-08-461-379A-2
11	462.5	49.7	202	2	US-08-462-390B-2
12	462.5	49.7	202	3	US-08-870-815-4
13	462.5	49.7	202	3	US-08-463-074B-2
14	462.5	49.7	202	3	US-08-465-585C-2
15	462.5	49.7	202	3	US-08-652-446-2
16	462.5	49.7	202	3	US-08-949-004-4
17	447	48.0	201	2	US-08-726-228-2
18	447	48.0	201	3	US-08-870-815-2
19	447	48.0	201	3	US-08-949-004-2
20	427.5	45.9	235	3	US-09-244-314-4
21	427.5	45.9	235	4	US-09-498-959-4
22	421.5	45.3	235	4	US-09-244-314-2
23	421.5	45.3	235	4	US-09-498-959-2
24	415.5	44.6	211	2	US-08-748-483-4
25	384	41.2	120	3	US-08-890-865A-11
26	382	41.0	120	3	US-08-890-865A-11
27	377	40.5	120	3	US-08-890-865A-11

28	374.5	40.2	121	2	US-08-588-258B-32	Sequence 32, Appl
29	374.5	40.2	121	3	US-08-460-505-32	Sequence 32, Appl
30	374.5	40.2	121	5	PCT-US96-08295-32	Sequence 32, Appl
31	351.5	37.8	196	2	US-08-829-110-5	Sequence 3, Appl
32	351.5	37.8	196	2	US-08-748-483-3	Sequence 3, Appl
33	351.5	37.8	196	4	US-09-702-705-339	Sequence 339, App
34	351.5	37.8	196	4	US-09-736-457-339	Sequence 339, App
35	351.5	37.8	196	4	US-09-614-124B-339	Sequence 339, App
36	351.5	37.8	196	4	US-09-671-235-339	Sequence 339, App
37	351.5	37.8	196	4	US-09-588-184-339	Sequence 339, App
38	351.5	37.8	196	4	US-09-658-824-339	Sequence 339, App
39	325.5	35.0	119	2	US-08-588-258B-31	Sequence 31, Appl
40	325.5	35.0	119	3	US-08-460-505-31	Sequence 31, Appl
41	323.5	34.7	119	5	PCT-US96-08295-31	Sequence 31, Appl
42	323.5	34.7	119	3	US-08-890-865A-15	Sequence 15, Appl
43	318	34.2	159	2	US-08-829-110-1	Sequence 11, Appl
44	298.5	32.1	68	2	US-08-588-258B-11	Sequence 11, Appl
45	298.5	32.1	68	3	US-08-460-505-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-08-748-483-1  
Sequence 1, Application US/08748483  
Patent No. 5955314  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08748,483  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0157 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 181 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: 57362  
US-08-748-483-1  
Query Match 100.0%; Score 931; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 8.6e-87;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 11:30:02 ; Search time 4859 Seconds

(without alignments)  
12681.537 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691

Sequence: 1 taagaagctgacttaaga.....tgcaaaaaaaaaaaaaa 1691

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1689.4	99.9	1714	3	CR619141 full-length
2	1689.4	99.9	2035	3	CR600297 full-length
3	1114.4	65.9	1456	3	CR613029 full-length
4	1113.4	65.8	1452	3	CR597576 full-length
5	1079.6	63.8	1147	5	BX425491
6	1079.4	63.8	1101	5	CR609141 full-length
7	1055.2	62.4	1101	5	BX446885
8	1033.6	61.1	1143	5	BX446297
9	1016.8	60.1	1099	1	AL515897
10	1011.4	59.8	1132	5	BX384451
11	1000.4	59.2	1002	3	CR625895 full-length
12	990	58.5	1096	3	BX403980
13	985.4	58.3	1000	3	CR617436 full-length
14	973.4	57.6	1092	1	AL517305
15	968	57.2	1177	5	BUS08112
16	958.2	56.7	998	1	AL516736
17	955	56.5	1073	5	BX458066
18	954.8	56.4	1054	5	BX425160
19	954.2	56.4	973	1	AL515896
20	946.4	55.0	1074	5	BX438124
21	945.8	55.9	1125	1	AL514350
22	945	55.9	1129	5	BX403854
23	939	55.5	1065	1	AL517317
24	938.2	55.5	1097	5	BX416594

25	935.2	55.3	1060	1	AL518711
26	932.6	55.2	1101	1	AL518211
27	932.2	55.1	1121	1	AL518726
28	931.4	55.1	1065	5	BX425274
29	928.4	54.9	1066	5	AL515561
30	927	54.8	1061	5	BX425161
31	923	54.6	1182	5	BUS08040
32	921.4	54.5	933	1	AL514762
33	901.6	53.3	1065	1	AL518255
34	896.4	53.0	1068	5	BX457536
35	888.8	52.6	1001	5	BX403989
36	888.6	52.5	990	1	AL514666
37	881.8	52.1	1074	1	AL518459
38	880	52.0	981	5	BQ719360
39	876	51.8	1132	5	BX446626
40	875.2	51.8	1136	1	AL518210
41	875	51.7	894	5	BX404056
42	871.2	51.5	912	1	AL514736
43	868	51.3	881	1	AL514802
44	866.6	51.2	1065	5	BX416045
45	864.8	51.1	1085	5	BX446930

## ALIGNMENTS

RESULT 1  
LOCUS: CR619141  
DEFINITION: full-length cDNA clone CLOB0112605 of Neuroblastoma of Homo sapiens (human).  
ACCESSION: CR619141  
VERSION: CR619141.1 GI:50499948  
KEYWORDS: HTC; CNSLT cDNA.  
SOURCE: Homo sapiens (human)  
ORGANISM: Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE: Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE: Full-length cDNA libraries and normalization  
JOURNAL: Unpublished  
REMARK: Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue  
2 (bases 1 to 1714)  
Genoscope.  
REFERENCE: Direct Submission  
AUTHORS: Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ;  
JOURNAL: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr  
COMMENT: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
FEATURES  
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location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="CLOB0112605"  
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/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 99.9%; Score 1689.4; DB 3; Length 1714;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TAAGAAGTGTACTTAAGCGAGAGCTAAGCCACCTGCAAAATGTGCAAGACTTG 60  
24 TAAGAAGTGTACTTAAGCGAGAGCTAAGCCACCTGCAAAATGTGCAAGACTTG 83

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 15:05:01 ; Search time 935 Seconds  
(without alignments)  
10391.762 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691

Sequence: 1 taagaagttgacttaagc.....tcgaataaaaaaaaaa 1691

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Published Applications NA.\*  
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3: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
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21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1691	100.0	1691	US-10-804-491-24	Sequence 24, Appl
2	1689.4	99.9	2076	US-10-240-425-345	Sequence 345, Appl
3	1678.4	99.3	5809	US-10-133-013-103	Sequence 103, Appl
4	1676.4	99.1	1923	US-10-411-224-55	Sequence 55, Appl
5	1676.4	99.1	1923	US-10-047-021-55	Sequence 55, Appl
6	1587.8	93.9	2190	US-10-641-643-795	Sequence 795, Appl
7	856.2	50.6	878	US-09-604-287A-82	Sequence 82, Appl
8	856.2	50.6	878	US-09-834-759-82	Sequence 82, Appl
9	856.2	50.6	878	US-09-339-338-82	Sequence 82, Appl
10	856.2	50.6	878	US-09-551-621-82	Sequence 82, Appl
11	856.2	50.6	878	US-10-007-805-82	Sequence 82, Appl
12	856.2	50.6	878	US-10-076-622-82	Sequence 82, Appl

13	856.2	50.6	878	15	US-10-124-805-82	Sequence 82, Appl
14	856.2	50.6	878	15	US-10-441-893-82	Sequence 82, Appl
15	720	42.6	744	9	US-09-206-639-2	Sequence 2, Appl
16	606.6	35.9	631	9	US-09-736-457-553	Sequence 553, Appl
17	606.6	35.9	631	9	US-09-902-941-553	Sequence 553, Appl
18	606.6	35.9	631	9	US-09-849-626-553	Sequence 553, Appl
19	606.6	35.9	631	10	US-09-476-100-553	Sequence 553, Appl
20	606.6	35.9	631	14	US-10-017-754-553	Sequence 553, Appl
21	606.6	35.9	631	15	US-10-113-872-553	Sequence 553, Appl
22	606.6	35.9	631	15	US-10-283-017-553	Sequence 553, Appl
23	601.4	35.6	607	14	US-10-175-523-35	Sequence 35, Appl
24	572.8	33.9	784	9	US-09-736-457-1658	Sequence 1658, Appl
25	572.8	33.9	784	9	US-09-902-941-1658	Sequence 1658, Appl
26	572.8	33.9	784	9	US-09-849-626-1658	Sequence 1658, Appl
27	572.8	33.9	784	14	US-10-017-754-1658	Sequence 1658, Appl
28	572.8	33.9	784	15	US-10-113-872-1658	Sequence 1658, Appl
29	572.8	33.9	784	15	US-10-283-017-1658	Sequence 1658, Appl
30	543.4	32.1	576	9	US-09-736-457-657	Sequence 657, Appl
31	543.4	32.1	576	9	US-09-902-941-657	Sequence 657, Appl
32	543.4	32.1	576	9	US-09-849-626-657	Sequence 657, Appl
33	543.4	32.1	576	10	US-09-476-100-657	Sequence 657, Appl
34	543.4	32.1	576	14	US-10-017-754-657	Sequence 657, Appl
35	543.4	32.1	576	15	US-10-113-872-657	Sequence 657, Appl
36	543.4	32.1	576	15	US-10-283-017-657	Sequence 657, Appl
37	516.4	30.5	571	11	US-09-969-034-2951	Sequence 2951, Appl
38	491.4	29.1	817	15	US-10-398-853-6	Sequence 6, Appl
39	456	27.0	457	16	US-10-242-535A-42596	Sequence 42596, A
40	456	27.0	457	16	US-10-085-783A-42596	Sequence 42596, A
41	442.8	26.2	543	15	US-10-398-853-2	Sequence 2, Appl
42	426.4	25.2	663	16	US-10-357-820-47	Sequence 47, Appl
43	423.8	25.1	427	10	US-09-918-995-5821	Sequence 5821, Appl
44	413	24.4	459	10	US-09-918-995-13701	Sequence 13701, A
45	383.8	22.7	411	10	US-09-918-995-17122	Sequence 17122, A

#### ALIGNMENTS

RESULT 1  
US-10-804-491-24  
Sequence 24, Application US/10804491  
Publication No. US20040180375A1  
GENERAL INFORMATION:  
APPLICANT: Cismowski, Mary  
APPLICANT: Duzic, Emir  
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor  
FILE REFERENCE: 60388-A-PCT-US  
CURRENT FILING DATE: 2004-03-19  
PRIORITY FILING DATE: 2004-03-19  
PRIOR APPLICATION NUMBER: US/09/709,103  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 24  
LENGTH: 1691  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (45)..(587)  
OTHER INFORMATION:  
US-10-804-491-24

Query Match: 100.0%; Score 1691; DB 17; Length 1691;

Best Local Similarity: 100.0%; Pred. No. 0;

Matches 1691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAGAAGTTGACTTAAGCGAGAGCTAAGCCACCTGCCAAATGTGCAAGACTTG 60  
DB 1 TAAGAAGTTGACTTAAGCGAGAGCTAAGCCACCTGCCAAATGTGCAAGACTTG 60  
QY 61 CAGCTTCCCTCATCATGCTGTAAGAGGCGCAAGAGATTAAATCAAGTTGGAATTC 120

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OM nucleic - nucleic search, using SW model

Run on: January 12, 2005, 11:46:42 ; Search time 163 Seconds

(without alignments)  
7373.890 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691

Sequence: 1 taagaagctgtacttaagc.....tcgcaaaaaaaaaaaaaa 1691

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*  
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5: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1691	100.0	1691	US-09-709-103-24	Sequence 24, App1
2	1691	100.0	1691	US-09-439-410A-24	Sequence 24, App1
3	1676.8	99.2	3208	US-09-566-921-111	Sequence 111, App
4	1587.8	93.9	2190	US-09-023-655-795	Sequence 795, App
5	856.2	50.6	878	US-09-222-575-82	Sequence 82, App1
6	856.2	50.6	878	US-09-389-681-82	Sequence 82, App1
7	856.2	50.6	878	US-09-620-405B-82	Sequence 82, App1
8	856.2	50.6	878	US-09-339-338-82	Sequence 82, App1
9	856.2	50.6	878	US-09-433-826B-82	Sequence 82, App1
10	856.2	50.6	878	US-09-604-287A-82	Sequence 82, App1
11	856.2	50.6	878	US-09-285-480-82	Sequence 82, App1
12	856.2	50.6	878	US-09-834-759-82	Sequence 82, App1
13	856.2	50.6	878	US-09-590-751A-82	Sequence 82, App1
14	720	42.6	744	US-08-748-483-2	Sequence 2, App1
15	606.6	35.9	631	US-09-702-705-553	Sequence 553, App
16	606.6	35.9	631	US-09-736-457-553	Sequence 553, App
17	606.6	35.9	631	US-09-614-124B-553	Sequence 553, App
18	606.6	35.9	631	US-09-671-325-553	Sequence 553, App
19	606.6	35.9	631	US-09-589-184-553	Sequence 553, App
20	606.6	35.9	631	US-09-658-824-553	Sequence 553, App
21	572.8	33.9	784	US-09-702-705-1658	Sequence 1658, App
22	572.8	33.9	784	US-09-736-457-1658	Sequence 1658, App
23	572.8	33.9	784	US-09-614-124B-1658	Sequence 1658, App
24	572.8	33.9	784	US-09-671-325-1658	Sequence 1658, App
25	572.8	33.9	784	US-09-658-824-1658	Sequence 1658, App
26	543.4	32.1	576	US-09-702-705-657	Sequence 657, App
27	543.4	32.1	576	US-09-736-457-657	Sequence 657, App

C 28	543.4	32.1	576	US-09-614-124B-657	Sequence 657, App
C 29	543.4	32.1	576	US-09-671-325-657	Sequence 657, App
C 30	543.4	32.1	576	US-09-589-184-657	Sequence 657, App
C 31	543.4	32.1	576	US-09-658-824-657	Sequence 657, App
C 32	379.2	22.4	399	US-09-702-705-491	Sequence 491, App
C 33	379.2	22.4	399	US-09-736-457-491	Sequence 491, App
C 34	379.2	22.4	399	US-09-614-124B-491	Sequence 491, App
C 35	379.2	22.4	399	US-09-671-325-491	Sequence 491, App
C 36	379.2	22.4	399	US-09-589-184-491	Sequence 491, App
C 37	379.2	22.4	399	US-09-658-824-491	Sequence 491, App
C 38	332.4	19.7	336	US-09-702-705-522	Sequence 522, App
C 39	332.4	19.7	336	US-09-736-457-522	Sequence 522, App
C 40	332.4	19.7	336	US-09-614-124B-522	Sequence 522, App
C 41	332.4	19.7	336	US-09-671-325-522	Sequence 522, App
C 42	332.4	19.7	336	US-09-589-184-522	Sequence 522, App
C 43	332.4	19.7	336	US-09-658-824-522	Sequence 522, App
C 44	191.8	11.3	800	US-09-016-434-1091	Sequence 1091, App
C 45	188.6	11.2	746	US-08-870-815-3	Sequence 3, App1

#### ALIGNMENTS

RESULT 1	US-09-709-103-24
Sequence 24, Application US/09709103	
Patent No. 6733991	
GENERAL INFORMATION:	
APPLICANT: Cismowski, Mary	
APPLICANT: Duzic, Emil	
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor	
FILE REFERENCE: 60388-A-PCT-US	
CURRENT APPLICATION NUMBER: US/09/709,103	
NUMBER OF SEQ ID NOS: 73	
SOFTWARE: PatentIn version 3.1	
SEQ ID NO 24	
LENGTH: 1691	
TYPE: DNA	
ORGANISM: Homo Sapiens	
FEATURE:	
NAME/KEY: CDS	
LOCATION: (45)..(587)	
OTHER INFORMATION:	
US-09-709-103-24	
Query Match	100.0%; Score 1691; DB 4; Length 1691;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1	TAAGAAGTTGTACTTAAGCGGAGGAGCTAAGCCACTGCGCAAAATGTCAGAAAGACTTG 60
DB 1	TAAAGAGTTGTACTTAAGCGGAGGAGCTAAGCCACTGCGCAAAATGTCAGAAAGACTTG 60
QY 61	CAGCTTGGCCCACTCATGCTGGAAGGCGCAAGAGATTAAAGTCAAGTTGGAAATTC 120
DB 61	CAGCTTGGCCCACTCATGCTGGAAGGCGCAAGAGATTAAAGTCAAGTTGGAAATTC 120
QY 121	TCTCTCAGAGGCAAGCTAGTTGTCATCTGTCATTCGTCATAGAGAGCCAGAGA 180
DB 121	TCTCTCAGAGGCAAGCTAGTTGTCATCTGTCATTCGTCATAGAGAGCCAGAGA 180
QY 181	AACCGAGGCAAGCCAGAAAACCTGCGTGAAGAGGCGCTGCAAGTGGGCTGCG 240
DB 181	AACCGAGGCAAGCCAGAAAACCTGCGTGAAGAGGCGCTGCAAGTGGGCTGCG 240
QY 241	ACAACTCTGAGAGCAACTAGTGAAGCTTCCAGTTTCAAAAGTTTCTGAAGTGAAT 300
DB 241	ACAACTCTGAGAGCAACTAGTGAAGCTTCCAGTTTCAAAAGTTTCTGAAGTGAAT 300
QY 301	TCAAGTGAAGAAACCTTGAAGTTGCTGAGAGTTTCAAGAGATCAAGTCCC 360
DB 301	TCAAGTGAAGAAACCTTGAAGTTGCTGAGAGTTTCAAGAGATCAAGTCCC 360

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:41:28 ; Search time 788 Seconds  
(without alignments)  
11264.938 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691  
Sequence: 1 taagaagtcgtacttaagc.....tcgcaaaaaaaaaaaaaa 1691

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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7: geneseqn2002bs:\*  
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12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1691	100.0	1691	3 AA236910	AA236910 cDNA enco
2	1689.4	99.9	2076	11 ADP65641	ADP65641 Human mRN
3	1689.4	99.9	2076	11 ADP65077	ADP65077 Human reg
4	1687.8	99.8	2075	10 ABX74396	ABX74396 Human cDN
5	1678.4	99.3	5809	10 ADI02562	ADI02562 Human cDN
6	1676.8	99.2	3208	12 ADI61743	ADI61743 Human cDN
7	1676.4	99.1	1923	2 AAX51745	AAX51745 DNA encod
8	1676.4	99.1	1923	6 ABO92597	ABQ92597 Human sec
9	1587.8	93.9	2180	11 ADI31146	ADI31146 Human cDN
10	163.8	74.7	10427	6 ABK69943	ABK69943 Human sec
11	856.2	50.6	878	4 AAF17597	AAF17597 Human bre
12	856.2	50.6	878	4 AAS47027	AAS47027 Human bre
13	856.2	50.6	878	6 ABK95062	ABK95062 Human bre
14	856.2	50.6	878	6 ABT08682	ABT08682 Human bre
15	856.2	50.6	878	6 ABS63626	ABS63626 Human bre
16	856.2	50.6	878	10 ABT32840	ABT32840 Human tum
17	856.2	50.6	878	11 ADI92744	ADI92744 Human bre
18	856.2	50.6	878	12 ADE44034	ADE44034 Human cDN
19	720	42.6	745	2 AAV38084	AAV38084 Human neu
20	632.6	37.4	934	4 AAI97782	AAI97782 Human lun
21	606.6	35.9	631	5 AAF66618	AAF66618 Human lun

22	606.6	35.9	631	6 ABK38529	ABK38529 cDNA enco
23	606.6	35.9	631	8 ACA10858	ACA10858 Human lun
24	606.6	35.9	631	8 ABX99809	ABX99809 Lung canc
25	606.6	35.9	631	10 ADH46072	ADH46072 Human lun
26	606.6	35.9	631	12 ADE71824	ADE71824 Human lun
27	596.4	35.3	955	4 AAI97781	AAI97781 Human neu
28	572.8	33.9	784	6 ABK39620	ABK39620 cDNA enco
29	572.8	33.9	784	6 ACA11949	ACA11949 Human lun
30	572.8	33.9	784	8 ACA03135	ACA03135 Lung canc
31	572.8	33.9	784	10 ADH47177	ADH47177 Human lun
32	543.4	32.1	576	5 AAF68722	AAF68722 Human lun
33	543.4	32.1	576	6 ABK38633	ABK38633 cDNA enco
34	543.4	32.1	576	8 ACA10962	ACA10962 Human lun
35	543.4	32.1	576	8 ABX99913	ABX99913 Lung canc
36	543.4	32.1	576	10 ADH46176	ADH46176 Human lun
37	543.4	32.1	576	12 ADE71928	ADE71928 Human lun
38	516.4	30.5	571	6 ABO59256	ABO59256 Human col
39	491.4	29.1	817	6 ABK99979	ABK99979 Rat disea
40	442.8	26.2	543	6 ABK99975	ABK99975 Rat disea
41	426.4	25.2	663	10 ADF44700	ADF44700 Human NOV
42	423.8	25.1	427	9 ACH18609	ACH18609 Human adu
43	423.2	25.0	663	12 ADO50885	ADO50885 Human NOV
44	413	24.4	459	9 ACH26489	ACH26489 Human adu
45	383.8	22.7	411	9 ACH29910	ACH29910 Human tes

## ALIGNMENTS

RESULT 1	AA236910	standard; cDNA; 1691 BP.
ID	AA236910	
XX	XX	
AC	AA236910;	
XX	XX	
DT	13-MAR-2000	(first entry)
XX	XX	
DE	cDNA encoding a regulator of G protein signalling RGSS.	
XX	XX	
KM	Activator of G protein signalling; AGS; ras-related G protein;	
KM	GTP hydrolysis; G protein activity; pheromone response pathway;	
KM	G protein-coupled signal transduction; G-gamma selectivity;	
KM	cellular signal transduction; regulator of G protein signalling; RGSS;	
se.		
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	45..590
FT	FT	/*tag= a
FT	FT	/product= "regulator of G-protein signalling"
XX	XX	
PN	W09958670-A1.	
XX	XX	
PD	18-NOV-1999.	
XX	XX	
PF	07-MAY-1999;	99WO-US010151.
XX	XX	
PR	08-MAY-1998;	98US-0084842P.
PR	07-OCT-1998;	98US-0103355F.
XX	XX	
PA	(CADU-) CADUS PHARM CORP.	
XX	XX	
PI	Cismowski M, Duzic E;	
XX	XX	
DR	WPI, 2000-072337/06.	
XX	XX	
DR	P-BSD; AAY53931.	
XX	XX	
PT	A new activator of G protein signalling used to treat disorders	
PT	characterized by an aberrant AGS protein activity.	
XX	XX	
PS	Claim 73; Page 139-140; 162pp; English.	
XX	XX	

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:32:26 ; Search time 112.522 Seconds  
(without alignments)  
895.854 Million cell updates/sec

Title: US-10-804-491-2

Perfect score: 1449

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: geneeqp2001s.\*  
5: geneeqp2002s.\*  
6: geneeqp2003as.\*  
7: geneeqp2003bs.\*  
8: geneeqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	100.0	281	2	AA142693
2	1449	100.0	281	3	AA153924
3	1449	100.0	281	3	AA153924
4	1449	100.0	281	6	ABR41059
5	1441	99.4	281	3	AA199656
6	1399.5	96.6	280	2	AA142694
7	893	61.6	278	3	AA153923
8	893	61.6	278	5	ABR90722
9	893	61.6	278	6	ABU54429
10	893	61.6	278	8	AD167005
11	893	61.6	278	8	ADQ17642
12	893	61.6	266	5	ABG59971
13	889	61.4	266	5	ABR90733
14	889	61.4	266	6	ABU54440
15	879	60.7	266	5	ABG70951
16	863	59.6	266	6	ABU54488
17	863	59.6	266	6	ABG26384
18	719	49.6	293	4	ABR60711
19	615	42.4	434	4	ABR60711
20	517	35.7	175	8	ABO58923
21	425	29.3	82	7	ADOC35028
22	334	23.1	199	4	AA139896
23	334	23.1	206	4	AAE23389
24	334	23.1	206	4	AA141682
25	330.5	22.8	319	4	ABR68087

26	327	22.6	214	7	ADE09235	Adc09235 Novel pro
27	326	22.5	198	6	ABU62878	Abu62878 Human ras
28	326	22.5	238	6	ABU11837	Abu11837 Human MDD
29	326	22.5	253	7	ABE08246	ABE08246 Novel pro
30	322	22.2	293	5	ABP51431	ABP51431 Human MDD
31	307.5	21.2	233	4	ABR63896	ABR63896 Drosophila
32	305	21.0	183	8	ADL35821	ADL35821 Human RAS
33	305	21.0	183	8	ADN05368	ADN05368 Antipso
34	305	21.0	215	4	AA100955	AA100955 Human bon
35	301	20.8	183	4	AA105076	AA105076 RALP1A
36	301	20.8	183	4	AA139413	AA139413 Human pol
37	301	20.8	183	6	ABU62883	ABU62883 Ras-famil
38	301	20.8	183	7	ADL14201	ADL14201 Human src
39	301	20.8	203	2	AA182591	AA182591 Human TC2
40	301	20.8	203	6	ABR41057	ABR41057 Human MAP
41	301	20.8	204	6	ABR41056	ABR41056 Human MAP
42	301	20.8	204	7	ADU69435	ADU69435 Human hea
43	301	20.8	204	8	ADL19894	ADL19894 Human PRO
44	301	20.8	204	8	ADL19631	ADL19631 Human PRO
45	301	20.8	288	4	AA174576	AA174576 Human col

## ALIGNMENTS

RESULT 1  
ID AAY42693  
ID AAY42693 standard; protein; 281 AA.

AC AAY42693;  
DT 17-JAN-2000 (first entry)

DE Human kd312 polypeptide.  
KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;  
KW heart attack; head trauma; neurodegenerative disease; human;  
KW Parkinson's disease; Alzheimer's disease.

OS Homo sapiens.  
FN MO9950288-A2.  
PD 07-OCT-1999.  
PF 30-MAR-1999; 99MO-US006993.  
FR 31-MAR-1998; 98US-00053374.  
(AMGE-) AMGEN INC.

PI Yen K;  
DR WPI: 1999-601322/51.  
DR N-PSDB; AA223022, AA223023.

PT kd312 polypeptides useful for treating diseases and disorders associated  
with alterations in cell proliferation and cell death.  
PS Claim 10; Fig 5; 85pp; English.  
XX The invention provides nucleic acid molecules encoding human and rat  
XX kd312 polypeptides. The kd312 polypeptides can be expressed by strand  
XX recombinant methodology. The kd312 sequences, and the antibodies against  
XX the proteins may be used to treat or diagnose the presence or progression  
XX of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),  
XX stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.  
XX Parkinson's disease and Alzheimer's disease). The present sequence  
XX represents the human kd312 polypeptide

Sequence 281 AA;  
SQ

Query Match 100.0%; Score 1449; DB 2; Length 281;



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OW protein - protein search, using sw model

Run on: January 12, 2005, 16:38:13 ; Search time 27.9784 Seconds  
(without alignments)  
966.351 Million cell updates/sec

Title: US-10-804-491-2  
Perfect score: 1449  
Sequence: 1 MKLAMIKMKCPDSELSIP.....IREKASAGQAKDKRCVTS 281

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: .pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314.5	21.7	217	1	TVWYRS
2	306	21.1	183	1	TVHUR2
3	303	20.9	219	2	T15833
4	301	20.8	183	2	S03180
5	296.5	20.8	203	1	TVHUC2
6	296.5	20.5	215	2	JUN0562
7	290.5	20.0	219	2	T45545
8	289.5	20.0	188	2	S65761
9	288.5	19.9	219	1	TVWYRS
10	288.5	19.9	425	2	T25549
11	287	19.8	186	2	A37355
12	286.5	19.8	192	2	S32042
13	285.5	19.7	186	2	TVDOBS
14	285.5	19.7	186	2	S11229
15	285.5	19.7	212	2	A53778
16	283.5	19.6	184	1	A34655
17	283.5	19.6	184	1	TVHUR1
18	283.5	19.6	184	2	P38625
19	283.5	19.6	184	2	A61216
20	283	19.5	188	1	TVMS2K
21	283	19.5	188	2	S34138
22	283	19.5	272	2	A34511
23	282.5	19.5	184	1	A31961
24	282.5	19.5	184	2	A32342
25	282	19.5	188	1	I58402
26	282	19.5	218	1	TVHUR
27	281	19.4	188	2	JC5154
28	281	19.4	213	2	S12892
29	280.5	19.4	184	2	A41217

30	280	19.3	188	1	TVHUK2K	transforming prote
31	280	19.3	188	2	S31720	transforming prote
32	279.5	19.3	193	2	S38362	Pora2 protein - s
33	279	19.3	219	1	TVBYR	ras-like protein 1
34	278.5	19.2	184	2	JC5155	rap1a protein - tu
35	276	19.0	188	2	T19507	hypothetical prote
36	275.5	19.0	189	1	TVCHRS	transforming prote
37	275.5	19.0	189	1	TVHUR	transforming prote
38	274.5	18.9	189	1	TVWYRS	transforming prote
39	274.5	18.9	241	1	TVWYRS	transforming prote
40	274	18.9	189	2	S33796	ras protein homolo
41	273.5	18.9	172	2	A54321	transforming prote
42	273.5	18.9	183	2	S05483	transforming prote
43	273.5	18.9	189	2	A43816	transforming prote
44	273.5	18.9	189	2	A25229	c-H-ras 1 protein
45	272.5	18.8	187	2	A60192	transforming prote

## ALIGNMENTS

## RESULT 1

TVWYRS  
Transforming protein ras - shiitake mushroom  
C:Species: Lentinula edodes (shiitake mushroom)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: J0619; J01296  
R:Horii, K.; Kajiwara, S.; Saito, T.; Miyazawa, H.; Katayose, Y.; Shishido, K.  
Gene 105, 91-96, 1991  
A:Title: Cloning, sequence analysis and transcriptional expression of a ras gene of the  
A:Reference number: J01296; M01D:92039023; PMID:1937010  
A:Accession: J0619  
A:Molecule type: DNA  
A:Residues: 1-217 <HOR>  
A:Cross-references: UNIPROT:P28775; GB:D00742; NID:G217947; PIDN:BA00642.1; PID:G217947  
A>Note: The source was designated as Lentinus edodes  
C:Genetics:  
A:Gene: ras  
A:Introns: 4/3; 20/1; 45/1; 72/2; 137/1; 176/3  
C:Superfamily: ras transforming protein; translation elongation factor Tu homology  
C:Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleol  
F:11-126/Domain: translation elongation factor Tu homology <RTU>  
F:17-24/Region: nucleotide-binding motif A (P-loop)  
F:123-126/Region: GTP-binding NKXD motif  
F:153-155/Region: GTP-binding SAK/L motif  
F:223-244/2123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #str  
F:214/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted  
F:214/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 21.7%; Score 314.5; DB 1; Length 217;  
Best Local Similarity 35.2%; Pred. No. 6.2e-18;  
Matches 80; Conservative 35; Mismatches 67; Indels 45; Gaps 7;

QY	25	YRMVILGSSKVGKTAIVSRFLTGAFEDAYPTTIEDFRKYSIRGEVYQDILDTSGNHP	84
DB	11	YKLVVGGGKSKALTIQFIQSHFVDEYDPTIEDSVKQCVIDDEVALDVLDTAQOE	70
QY	85	FPNARRSLITNGDPIFVPSLDNRDSFEVQRLQQLDTRKSLCKTKTKENVPLVYICG	144
DB	71	YGARRDQYMRGTGEFLVYSITRSNSEEISTHQQL-----RVKQDTPPVVVA	122
QY	145	NKGDRDFYREVDREIEQLVGDDPQR---CAVEISAKKNSLIDQMFALFAAKLPSEM	201
DB	123	NKCDLEVERGVNME-----GRDLAHFGCKPFTSKRVINVDQAFQ-----	165
QY	202	SPDLHRRVSVQYCDVLAHKALRNKKLIRAG---SGGGGSDPGDARF	244
DB	166	--DIVREIR-KY-----NKEQQTGRMNTGGGGGPPPTVAG	199

## RESULT 2

TVHUR2  
Transforming protein rap2b - human

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:46:36 ; Search time 6984 Seconds  
(without alignments)  
11450.012 Million cell updates/sec

Title: US-10-804-491-24  
Perfect score: 1691  
Sequence: 1 taagaagctgacttaaac.....tcgcaaaaaaaaaaaaaa 1691

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_ph:\*  
7: gb\_pl:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_stg:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1691	100.0	1691	9	AF159570 Homo sapi
2	1689.4	99.9	2076	9	AB008109 Homo sapi
3	1689.4	99.9	5683	9	BSM805729
4	1687.8	99.8	2075	6	CO714475 Sequence
5	1686.4	99.7	2601	11	BV180396
6	1676.8	99.2	3208	6	AR454638
7	1676.4	99.1	1923	6	BD074349
8	1675.4	99.1	1710	6	BC030059
9	1587.8	93.9	2190	6	AR380250
10	1263.8	74.7	165329	9	AL583850
11	1263.8	74.7	191689	2	AC031977
12	1105.2	65.4	1285	9	AF030108
13	856.2	50.6	878	6	AR280577
14	856.2	50.6	878	6	AR283073
15	856.2	50.6	878	6	AR341846
16	856.2	50.6	878	6	AR343841
17	856.2	50.6	878	6	AR351042
18	856.2	50.6	878	6	AR352808
19	856.2	50.6	878	6	AR453622

20	856.2	50.6	878	6	AX302762	AX302762 Sequence
21	825.6	48.8	2078	4	SSC549925	h549925 Sus scrofa
22	720	42.6	744	6	AR075100	AR075100 Sequence
23	720	42.6	744	6	BD091623	BD091623 Human reg
24	684.4	40.5	857	11	BV166677	BV166677 RGS5_786
25	632.6	37.4	934	6	BD021619	BD021619 Novel gen
26	632.6	37.4	934	6	BD101557	BD101557 Novel gen
27	606.6	35.9	631	6	AR272824	AR272824 Sequence
28	606.6	35.9	631	6	AR276405	AR276405 Sequence
29	606.6	35.9	631	6	AR406680	AR406680 Sequence
30	606.6	35.9	631	6	AR440530	AR440530 Sequence
31	606.6	35.9	631	6	AR472688	AR472688 Sequence
32	606.6	35.9	631	6	AX062926	AX062926 Sequence
33	606.6	35.9	631	6	AX367843	AX367843 Sequence
34	596.4	35.3	955	6	BD021618	BD021618 Novel gen
35	596.4	35.3	955	6	BD101556	BD101556 Novel gen
36	572.8	33.9	784	6	AR273915	AR273915 Sequence
37	572.8	33.9	784	6	AR277496	AR277496 Sequence
38	572.8	33.9	784	6	AR407771	AR407771 Sequence
39	572.8	33.9	784	6	AR441621	AR441621 Sequence
40	572.8	33.9	784	6	AX368948	AX368948 Sequence
41	546	32.3	546	9	AF493929	AF493929 Homo sapi
42	543.4	32.1	576	6	AR272928	AR272928 Sequence
43	543.4	32.1	576	6	AR276509	AR276509 Sequence
44	543.4	32.1	576	6	AR406784	AR406784 Sequence
45	543.4	32.1	576	6	AR440634	AR440634 Sequence

## ALIGNMENTS

RESULT 1  
AF159570  
LOCUS  
DEFINITION Homo sapiens regulator of G-protein signalling 5 (RGS5) mRNA.  
ACCESSION AF159570  
VERSION AF159570.1 GI:5230675  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Fuenkranz, H., Lanier, S.M. and Duzic, E.  
TITLE Genetic screens in yeast to identify mammalian nonreceptor modulators of G-protein signaling  
JOURNAL Nat. Biotechnol. 17 (9), 878-883 (1999)  
MEDLINE 99403338  
PUBMED 10471929  
REFERENCE 2 (bases 1 to 1691)  
AUTHORS Cismowski, M.J. and Duzic, E.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUN-1999) Receptor Pharmacology/Biochemistry, Cadus Pharmaceutical Corporation, 777 Old Saw Mill River Road, Tarrytown, NY 10591, USA  
FEATURES  
source  
gene  
CDS  
location/Qualifiers  
1..1691  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cfeature\_type="liver"  
/dev stage="adult"  
1..1691  
/gene="RGS5"  
45..590  
/gene="RGS5"  
/codon\_start=1  
/product="regulator of G-protein signalling 5"  
/protein\_id="A040957.1"  
/db\_xref="GI:5230676"  
/translation="MCKGLALPHSCERAKEIKIKIGILLQKPDSDVIVYNEKP"

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:32:21 ; Search time 114.955 Seconds

(without alignments)  
1406.471 Million cell updates/sec

Title: US-10-804-491-2

Perfect score: 1449

Sequence: 1 MRLAMIKMKCPDSELSIP.....IREKASAGSQAXDKERCVIS 281

Scoring table: BLOSUM62

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1449	100.0	281	1 RASD_HUMAN	O9Y272 homo sapien
2	1405.5	97.0	280	1 RASD_MOUSE	O35626 mus musculu
3	1399.5	96.6	280	1 RASD_RAT	O9JX88 rattus norv
4	1144.5	79.0	265	1 O6PHV8	O6PHV8 brachydanio
5	1144.5	79.0	265	2 AAH56272	AAH56272 brachydan
6	996	68.7	154	2 O9HC43	O9HC43 homo sapien
7	896	61.8	266	2 O6GM99	O6GM99 xenopus lae
8	889	61.4	266	1 RHES_HUMAN	O96d21 homo sapien
9	889	61.4	266	2 CAG30363	CAG30363 homo sapi
10	867	59.8	317	2 O8JZW1	O8JZW1 mus musculu
11	863	59.6	266	1 RHES_MOUSE	O9WV43 mus musculu
12	615	42.4	454	2 O9VSI0	O9VSI0 drosophila
13	359	24.8	306	2 O9WSG7	O9WSG7 drosophila
14	352.5	24.3	278	2 O7OHQ9	O7OHQ9 anopheles g
15	341	23.5	199	2 O6GM41	O6GM41 xenopus lae
16	339	23.4	195	2 O803Y2	O803Y2 brachydanio
17	335	23.1	199	2 O9SKD9	O9SKD9 macaca fasc
18	334	23.1	199	2 O96H08	O96H08 homo sapien
19	334	23.1	199	2 O7TQ15	O7TQ15 mus musculu
20	326	22.5	198	2 O9V507	O9V507 homo sapien
21	325.5	22.5	198	2 O9V986	O9V986 drosophila
22	325.5	22.5	198	2 AAF57410	AAF57410 drosophila
23	321	22.2	198	2 AAH57556	AAH57556 mus muscu
24	318.5	22.0	280	2 O8WQD0	O8WQD0 drosophila
25	314.5	21.7	1	1 RASD_LENED	P28775 leninfuila e
26	312.5	21.6	332	2 O02139	O02139 caenorhabdi
27	309	21.3	182	2 O6NSJ3	O6NSJ3 xenopus lae
28	309	21.3	182	2 O7SV59	O7SV59 brachydanio
29	309	21.3	182	2 AAH70538	AAH70538 xenopus l
30	309	21.3	182	2 AAH70538	AAH70538 xenopus l
31	309	21.3	182	2 AAH70538	AAH70538 xenopus l

## ALIGNMENTS

32	309	21.3	182	2	AAH35575	AAH35575 xenopus 1
33	308.5	21.3	209	2	O8AYE6	O8AYE6 xenopus lae
34	307.5	21.2	233	2	O9VH66	O9VH66 drosophila
35	305	21.0	183	1	RP2B_HUMAN	P61225 mus sapien
36	305	21.0	183	1	RP2B_MOUSE	P61227 mus musculu
37	305	21.0	183	1	RP2B_RAT	P61227 rattus norv
38	305	21.0	183	2	O6NRU1	O6NRU1 xenopus lae
39	305	21.0	183	2	O7ZX67	O7ZX67 xenopus lae
40	305	21.0	183	2	AAH46528	AAH46528 mus muscu
41	305	21.0	183	2	BAC31411	BAC31411 mus muscu
42	305	21.0	183	2	BAC32189	BAC32189 mus muscu
43	305	21.0	183	2	AAH70626	AAH70626 xenopus 1
44	305	21.0	183	2	AAH35578	AAH35578 xenopus 1
45	303	20.9	183	2	O9BTS0	O9BTS0 homo sapien

## RESULT 1

RASD\_HUMAN STANDARD; PRT; 281 AA.

AC O9Y272; O9NYB4; 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Dexamethasone-induced Ras-related protein 1 (Activator of G-protein

signaling 1).

GN Name=RASD1; Synonyms=DEXRASI, AGS1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pituitary;

RA Kempainen R.J.;

RT "Identification of human pituitary Dextral.,"

RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.

RC MEDLINE=20135605; PubMed=10673050; DOI=10.1016/S0167-4781(99)00197-9;

RA Tu Y., Wu C.;

RT "Cloning, expression and characterization of a novel human Ras-related

protein that is regulated by glucocorticoid hormone.,"

RL Biochim. Biophys. Acta 1489:452-456(1999).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=9403338; PubMed=10471929;

RA Cismowski M.J., Takesono A., Ma C., Lizano J.S., Xie X.,

RA Pienkranz H., Lanier S.M., Duzic E.;

RT "Genetic screens in yeast to identify mammalian nonreceptor modulators

of G-protein signaling.,"

RL Nat. Biotechnol. 17:878-883(1999).

RN [4]

RP SEQUENCE FROM N.A.

RC Cismowski M.J., Xie X., Duzic E.;

RT "Genomic sequence of the human ras-related G-protein activator AGS1.,"

RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC Kempainen R.J., Behrend E.N.;

RT "Human Dextral gene.,"

RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Puhl H.L., Ikeda S.R., Aronstam R.S.;

RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:34:53 ; Search time 678.171 Seconds  
(without alignments)  
149.700 Million cell updates/sec

Title: US-10-804-491-2

Perfect score: 1449

Sequence: 1 MKLAMIKMCPSELSIP.....IREKASAGSQAKXKRCVIS 281

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1449	100.0	281	US-10-197-666A-88	Sequence 88, App1
2	1449	100.0	281	US-10-804-491-2	Sequence 2, App1
3	1449	100.0	281	US-10-804-491-4	Sequence 4, App1
4	1449	100.0	281	US-10-804-491-46	Sequence 46, App1
5	893	61.6	278	US-09-918-715-118	Sequence 178, App1
6	893	61.6	278	US-10-804-491-41	Sequence 41, App1
7	893	61.6	278	US-10-474-794-178	Sequence 178, App1
8	893	61.6	278	US-10-723-860-459	Sequence 459, App1
9	889	61.4	266	US-09-778-963A-4	Sequence 4, App1
10	889	61.4	266	US-09-918-715-198	Sequence 198, App1
11	879	60.7	266	US-10-474-794-198	Sequence 198, App1
12	879	60.7	266	US-09-778-963A-2	Sequence 2, App1
13	863	59.6	266	US-09-778-963A-5	Sequence 5, App1

14	863	59.6	266	10	US-09-918-715-293	Sequence 293, App
15	863	59.6	266	17	US-10-474-794-293	Sequence 293, App
16	517	35.7	175	14	US-10-029-386-32557	Sequence 32557, A
17	334	23.1	199	16	US-10-399-455-16	Sequence 16, App1
18	326	22.5	198	10	US-09-873-546-5	Sequence 5, App1
19	322	22.2	293	16	US-10-363-829-453	Sequence 453, App
20	305	21.0	183	15	US-10-231-956A-429	Sequence 429, App
21	303	20.9	219	14	US-10-369-493-5393	Sequence 5393, App
22	301	20.8	183	9	US-09-482-520A-8	Sequence 8, App1
23	301	20.8	183	9	US-09-873-546-12	Sequence 12, App1
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25	301	20.8	204	14	US-10-197-666A-82	Sequence 82, App1
26	301	20.8	204	16	US-10-408-765A-1241	Sequence 1241, App
27	301	20.8	204	16	US-10-322-281-474	Sequence 474, App
28	301	20.8	204	17	US-10-788-792-208	Sequence 208, App
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30	301	20.8	214	16	US-10-322-281-467	Sequence 467, App
31	301	20.8	288	14	US-10-106-698-5350	Sequence 5350, App
32	301	20.8	734	15	US-10-344-404-31	Sequence 31, App1
33	301	20.8	758	15	US-10-344-404-36	Sequence 36, App1
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41	283.5	19.6	184	16	US-10-408-765A-856	Sequence 856, App
42	283.5	19.6	184	16	US-10-322-281-78	Sequence 78, App1
43	283	19.5	188	16	US-10-738-646A-5	Sequence 5, App1
44	283	19.5	272	14	US-10-369-493-21983	Sequence 21983, A
45	282.5	19.5	184	10	US-09-873-546-11	Sequence 11, App1

#### ALIGNMENTS

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US-10-197-666A-88  
; Sequence 88, Application US/10197666A  
; Publication No. US20030092037A1  
; GENERAL INFORMATION:  
; APPLICANT: ASAHI KASEI KABUSIKI KAISYA  
; TITLE OF INVENTION: Elki phosphorylation related gene  
; FILE REFERENCE: PH-1548US  
; CURRENT APPLICATION NUMBER: US/10/197,666A  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: JP 2001-218204  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: JP 2001-263450  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: JP 2002-012176  
; PRIOR FILING DATE: 2002-01-21  
; PRIOR APPLICATION NUMBER: US 60/305,884  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/316,304  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: US 60/350,027  
; PRIOR FILING DATE: 2002-01-23  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 88  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-197-666A-88

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Best Local Similarity 100.0%; Pred. No. 3,7e-133;  
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1 MKLAMIKMCPSELSIPAKNCNRMVITLSSKVGKTAIYSRPLTGFEDATPTTIDF 60  
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OW protein - protein search, using sw model

Run on: January 12, 2005, 18:15:29 ; Search time 35.8653 seconds  
(without alignments)  
519.304 Million cell updates/sec

Title: US-10-804-491-2  
Perfect score: 1449  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1449	100.0	281	US-09-053-374A-2	Sequence 2, Appli
2	1449	100.0	281	US-09-709-103-2	Sequence 2, Appli
3	1449	100.0	281	US-09-709-103-4	Sequence 4, Appli
4	1449	100.0	281	US-09-709-103-46	Sequence 46, Appli
5	1449	100.0	281	US-09-439-410A-2	Sequence 2, Appli
6	1449	100.0	281	US-09-439-410A-4	Sequence 4, Appli
7	1449	100.0	281	US-09-439-410A-46	Sequence 46, Appli
8	1399.5	96.6	280	US-09-053-374A-5	Sequence 5, Appli
9	893	61.6	278	US-09-709-103-41	Sequence 41, Appli
10	893	61.6	278	US-09-439-410A-41	Sequence 41, Appli
11	311	21.5	60	US-09-439-410A-109	Sequence 109, App
12	306	21.1	183	US-08-531-525-39	Sequence 39, Appli
13	306	21.1	183	US-08-718-270A-39	Sequence 39, Appli
14	305	22.0	60	US-09-439-410A-82	Sequence 82, Appli
15	303	20.9	59	US-09-439-410A-91	Sequence 91, Appli
16	301	20.8	183	US-09-482-520A-8	Sequence 8, Appli
17	301	20.8	204	US-09-078-317-14	Sequence 14, Appli
18	301	20.8	204	US-09-454-818-14	Sequence 14, Appli
19	300	20.7	204	US-08-247-946A-4	Sequence 4, Appli
20	300	20.7	204	PCT-US95-06420-4	Sequence 4, Appli
21	296.5	20.5	215	US-08-531-525-49	Sequence 49, Appli
22	296.5	20.5	215	US-08-718-270A-49	Sequence 49, Appli
23	288	19.9	213	US-09-503-505A-3	Sequence 3, Appli
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25	286.5	19.8	184	US-08-718-270A-40	Sequence 40, Appli
26	285	19.7	187	US-09-078-317-11	Sequence 11, Appli
27	283	19.5	55	US-09-439-410A-117	Sequence 117, App

28	282	19.5	183	3	US-09-078-317-13	Sequence 13, Appli
29	282	19.5	183	4	US-09-454-818-13	Sequence 13, Appli
30	282	19.5	210	3	US-09-053-374A-7	Sequence 7, Appli
31	281	19.4	218	1	US-08-247-946A-3	Sequence 3, Appli
32	281	19.4	218	5	PCT-US95-06420-3	Sequence 3, Appli
33	280.5	19.4	218	2	US-08-531-525-43	Sequence 43, Appli
34	280.5	19.4	184	2	US-08-718-270A-43	Sequence 43, Appli
35	277.5	19.2	189	2	US-08-884-866A-3	Sequence 3, Appli
36	277.5	19.2	189	3	US-08-884-866A-6	Sequence 6, Appli
37	276	19.0	188	2	US-08-429-964-84	Sequence 84, Appli
38	275.5	19.0	160	3	US-08-884-866A-7	Sequence 7, Appli
39	275.5	19.0	183	4	US-09-765-298A-26	Sequence 26, Appli
40	275.5	19.0	186	1	US-08-077-256-3	Sequence 3, Appli
41	275.5	19.0	186	1	US-08-259-672-3	Sequence 3, Appli
42	275.5	19.0	186	1	US-08-459-331-3	Sequence 3, Appli
43	275.5	19.0	186	1	US-08-460-533-3	Sequence 3, Appli
44	275.5	19.0	186	5	PCT-US94-0665A-3	Sequence 3, Appli
45	275.5	19.0	189	3	US-09-209-668-11	Sequence 11, Appli

## ALIGNMENTS

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US-09-053-374A-2
; Sequence 2, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-053-374A-2
;
Query Match      100.0%; Score 1449; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.1e-148;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 MKLAMIKMCPSDSELSIPAKNCYRVVILGSSKVGKTAIVSRFLTGRFEDATPTEDF 60
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DB      61 HRKFTSIRGEVYQDIDITSGNHPFAMRRLSITGDVFLIVSLDRDSFEFVQRQQ 120
QY      121 ILDTFSCLKNTKENVDPVLYICGNKGRDPYREVDREIQLVGDGDPQCAVFEISAKK 180
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